

1  
g t t t a a t t a c c c a a g t t t g a g a t g g a c a a a t a t c a a a a t g t t c a a c a a a a g t c t g t c t t  
M D K Y Q N V Q Q K V C L

61  
g t a g t t a t t g a t g g a t g g c c t t t c c g a t g a a c a a c a c g g g a a t g c a a t t g c t a a a g c t  
V V I D G W G L S D E Q H G N A I A K A

121  
a a a a c g c c t a t t a t g g a c a a a c t t t g t t c t g g a a a t t g g c a a a a t t g g a g c a c a c g g t  
K T P I M D K L C S G N W Q K L E A H G

181  
c t t c a t g t t g g a t t g c c a g a a g g c t t a a t g g a a a t t c t g a a g t t g g a c a t t t g a a t a t a  
L H V G L P E G L M G N S E V G H L N I

241  
g g a g c t g g a a g a g t t a t t a t c a a g a t a t t g t t c g a a t t a a t t t g g c t g t t c a a c g a a a c  
G A G R V I Y Q D I V R I N L A V Q R N

301  
g a g t t t g t t a c a a a t c c t c a g a t t g t t g c a t c a g c t g a g c g t g c a a a g a a g g g a g t g g t  
E F V T N P Q I V A S A E R A K K G S G

361  
c g a t t g c a t t t a t t a g g a c t g g t t a g c g a t g g t g g t g t c c a c t c t c a t a t t g a t c a t c t t  
R L H L L G L V S D G G V H S H I D H L

421  
t t t g c g t t g a t a c g t g c a t t t a a a c a a t t a c a a g g t t t t c a t t c a c t t t t t t  
F A L I R A F K Q L Q V P K V F I H F F

481  
g c t g a t g g t c g a g a t a c t t c g c c a a c a a g t g g a g c t g g t t a t c t t g a a c a a c t t c t t c a a  
A D G R D T S P T S G A G Y L E Q L L Q

541  
t t t a t t g c t t c g g a a a g t a c g g a g a a t t g c t a c t a t t a c t g g a c g t t a t t a t g c a a t g  
F I A S E K Y G E L A T I T G R Y Y A M

601  
g a t a g g g a c a a a g a t g g a g a g c g t a t t a a g a t g g c t t a t g a g c a a t t g t t g g a g g t a t t  
D R D K R W E R I K M A Y E A I V G G I

661  
g g a c a a a a a g c c a c c g t t g a t a a g g c t g t c g a t g t t g t t a g a g a g c g a t a t g c t c a a t c t  
G Q K A T V D K A V D V V R E R Y A Q S

721  
g a g a c t g a c g a a t t t c t g a a a c c a a t t g t t t t t c g g a c g a t g g g c g a g t a a a g a t g a c  
E T D E F L K P I V F S D D G R V K D D

781  
g a t a c t c t t a t t t t c a a t t a t c g t g c t g a t c g t a t g c g t c a a a t t t g t g a a t g t t t g  
D T L I F F N Y R A D R M R Q I C E C L

841  
g g t c t c g a a c g t t a t a a a g a t c t t a a t a g t t c g g t t c c t c a c c c t a a a a a t a t t c a g a t t  
G L E R Y K D L N S S V P H P K N I Q I

FIGURE 1A

901  
 AGT GGG ATG ACC CAA TAC AAT AAA GAG TTT CCA TTT CCA TCG TTA TTC CCA CCT GTG ACT  
 S G M T Q Y N K E F P F P S L F P P V T

961  
 CAT ACT AAT GTG CTT GCT GAA TGG CTT GCT TCT CAA GGA GTT ACT CAA TTT CAC TGT GCG  
 H T N V L A E W L A S Q G V T Q F H C A

1021  
 GAA ACT GAG AAG TAT CCT CAT GTT ACC TTC TTC TTT AAT GGT GGT CGA GAA GTT CAA TTC  
 E T E K Y P H V T F F F N G G R E V Q F

1081  
 CAA GAT GAA GAG CGT TGT ATG GTT CCG TCA CCA AAA GAA GTT GCT ACA TAT GAT TTA AAA  
 Q D E E R C M V P S P K E V A T Y D L K

1141  
 CCA GAA ATG AAT GCT GCT GGA GTT GCC GAA AAA ATG GTC GAG CAA ATT GAG TCA GGC AGG  
 P E M N A A G V A E K M V E Q I E S G R

1201  
 CAT CCT TTG GTT ATG TGC AAT TTT GCG CCT CCT GAC ATG GTT GGA CAT ACT GGT AAA TTT  
 H P L V M C N F A P P D M V G H T G K F

1261  
 GAA CCT GCC GTC AAA GCA TGT CAA GCT ACT GAC GAG GCA ATT GGA AAG ATA TTT GAA GCA  
 E P A V K A C Q A T D E A I G K I F E A

1321  
 TGC CAA ACT TAT AAT TAC GTT CTT ATG GTT ACT TCC GAT CAT GGA AAT GCT GAG AAG ATG  
 C Q T Y N Y V L M V T S D H G N A E K M

1381  
 ATT GCT CCC GAT GGT AGT GAA CAT ACT GCA CAT ACC TGC AAT TTG GTC CCA TTT ACT TGC  
 I A P D G S E H T A H T C N L V P F T C

1441  
 TCT TCC AAA ACA TTT GTT TTT AAA TCG ACT CCA CCT ACT GGA GAT GAT GGC AAA GAA CGT  
 S S K T F V F K S T P P T G D D G K E R

1501  
 GCA CGA GCC TTA CGT GAT GTT GCA CCG ACT GTT CTA CAA TTA ATG GGC TTA CCT GTA CCG  
 A R A L R D V A P T V L Q L M G L P V P

1561  
 CCG GAG ATG GAT GGC GTT CCT TTA CTT GAA CAG AGA GGA TAA gaa gtt aat tga caa tag  
 P E M D G V P L L E Q R G \*

1621  
 gaa ata aat atg agc tgc tat tac aag caa ttt taa aaa ttt tag taa aac gag taa ttt

1681  
 ttg ata tat aca tat tta gaa atc tcc gtt ata aaa att

FIGURE 1B

1  
Met phe val ala leu gly ala gln ile tyr arg gln tyr phe gly arg arg gly met ala  
21  
met ala asn asn ser ser val ala asn lys val cys leu ile val ile asp gly trp gly  
41  
val ser glu asp pro tyr gly asn ala ile leu asn ala gln thr pro val met asp lys  
61  
leu cys ser gly asn trp ala gln ile glu ala his gly leu his val gly leu pro glu  
81  
gly leu met gly asn ser glu val gly his leu asn ile gly ala gly arg val ile tyr  
101  
gln asp ile val arg ile asn leu ala val lys asn asn lys phe val thr asn glu ser  
121  
leu val asp ala cys asp arg ala lys asn gly asn gly arg leu his leu ala gly leu  
141  
val ser asp gly gly val his ser his ile asp his met phe ala leu val lys ala ile  
161  
lys glu leu gly val pro glu leu tyr leu his phe tyr gly asp gly arg asp thr ser  
181  
pro asn ser gly val gly phe leu glu gln thr leu glu phe leu glu lys thr thr gly  
201  
tyr gly lys leu ala thr val val gly arg tyr tyr ala met asp arg asp asn arg trp  
221  
glu arg ile asn val ala tyr glu ala met ile gly gly val gly glu thr ser asp glu  
241  
ala gly val val glu val val arg lys arg tyr ala ala asp glu thr asp glu phe leu  
261  
lys pro ile ile leu gln gly glu lys gly arg val gln asn asp asp thr ile ile phe  
281  
phe asp tyr arg ala asp arg met arg glu ile ser ala ala met gly met asp arg tyr  
301  
lys asp cys asn ser lys leu ala his pro ser asn leu gln val tyr gly met thr gln  
321  
tyr lys ala glu phe pro phe lys ser leu phe pro pro ala ser asn lys asn val leu  
341  
ala glu trp leu ala glu gln lys val ser gln phe his cys ala glu thr glu lys tyr  
361  
ala his val thr phe phe phe asn gly gly leu glu lys gln phe glu gly glu glu arg  
381  
cys leu val pro ser pro lys val ala thr tyr asp leu gln pro glu met ser ala ala  
401  
gly val ala asp lys met ile glu gln leu glu ala gly thr his pro phe ile met cys  
421  
asn phe ala pro pro asp met val gly his thr gly val tyr glu ala ala val lys ala  
441  
cys glu ala thr asp ile ala ile gly arg ile tyr glu ala thr gln lys his gly tyr

FIGURE 2A

**FIGURE 2B**

1 *M.incognita* PGM  
 2 *C.elegans* PGM

1 .....MDKYQNVQKVCGLVLDGCGTSDQHGNATAKAKTPTMDR: 40  
 2 MFVALGAQIYRQYFGRRGMAANNSSVANKVCLHVIDGCGVSEDPTGNATLNAQTPVMDK: 60

1 LCSGNWQKLEAHGLHVGLEPGCLMGNSEVGHNLNIGAGRVIYODIVRLNLAVORNEEVLNPQ:100  
 2 LCSGNWAQLEAHGLHVGLEPGCLMGNSEVGHNLNIGAGRVIYODIVRLNLAVKNNKEVLNES:120

1 IVASAEKAKKSGRIHLLGLVSDGGVHSHIDHLEALIRAFKQLOVKKVETHEPADGRDTS:160  
 2 LVDACDRAKNGNCRHLHLAGLVSDGGVHSHIDHMEALVKAIKELGVVEETHEFGDGRDTS:180

1 PTSGAGYLEOLLQPTASEK.VGELATITGRYAMDRDKRHERKMAVEATVGGTCQKATV:219  
 2 ENSGVCELEOTLEETREKTTGKGLATVVGRYAMDRDNKWERINVAEAMEGGVGETSDE:240

1 DKAMDVVRERYAQSEETDEFLKPLVFS.DDGRVKDDDTLLENNRADRMROLCECEGTERY:278  
 2 AGVVEVVRKRYAADETDEFLKPLILQGEKERVONDDTLLEFFDTRADRMREISAAAMGMDRY:300

1 KDLNLSMPHPKNTQISGMTQYNKEPPEPSLEPPVLDHTNVLAEWLASQGVTOFHCAETEKY:338  
 2 KDCNSKLAHPSNLQVYGMTQYKAEPEKSLEPPASNKNVLAEWLAEDKVSOFHCAETEKY:360

1 PHVTFFENGGRVQFQDEERCMVPSKPEVATYDIKPEMNAGVAEKMWEOLESGRHPLVM:398  
 2 AVVTFFENGGLKQFEGEERCLVPSK.VATYDIQPRMSAAGVADKMTQETAGTHBFILM:419

1 CNEAPPDMVGHTGKEEPAYKACQTDGAGKTEACOTYNVLMVDSHGNAEKMIAPDG:458  
 2 CNEAPPDMVGHTGVCEAAVKACEATDIATGRITYEATOKHGISLMVADHGNAEKMKAPDG:479

1 SEHTAHTCNLVFDCSSKTEVVKSTPPTGDDGKERARALRDVADPWLOLMGLEVPPEMDG:518  
 2 GKHTAHTCYRQPLTLSPGGEKTVDP.....ADRHPLCDVADPWLAEMGLEQPAEMTG:532

1 MPLEQRG:526  
 2 VSLVQKIZ:539

FIGURE 3